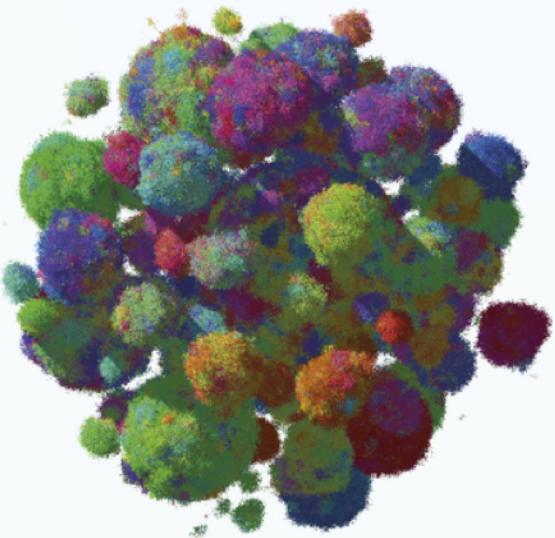


# Predicting tumor growth using a statistical layered population abstraction

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Joint work with Gregory Batt and Blaise Genest

# Tumor Model



## Tumor Simulator

[B. Waclaw, I. Bozic, M. Pittman, R. Hruban, B. Vogelstein & M. Nowak, 2016, A spatial model predicts that dispersal and cell turnover limit intratumour heterogeneity, *Nature*]

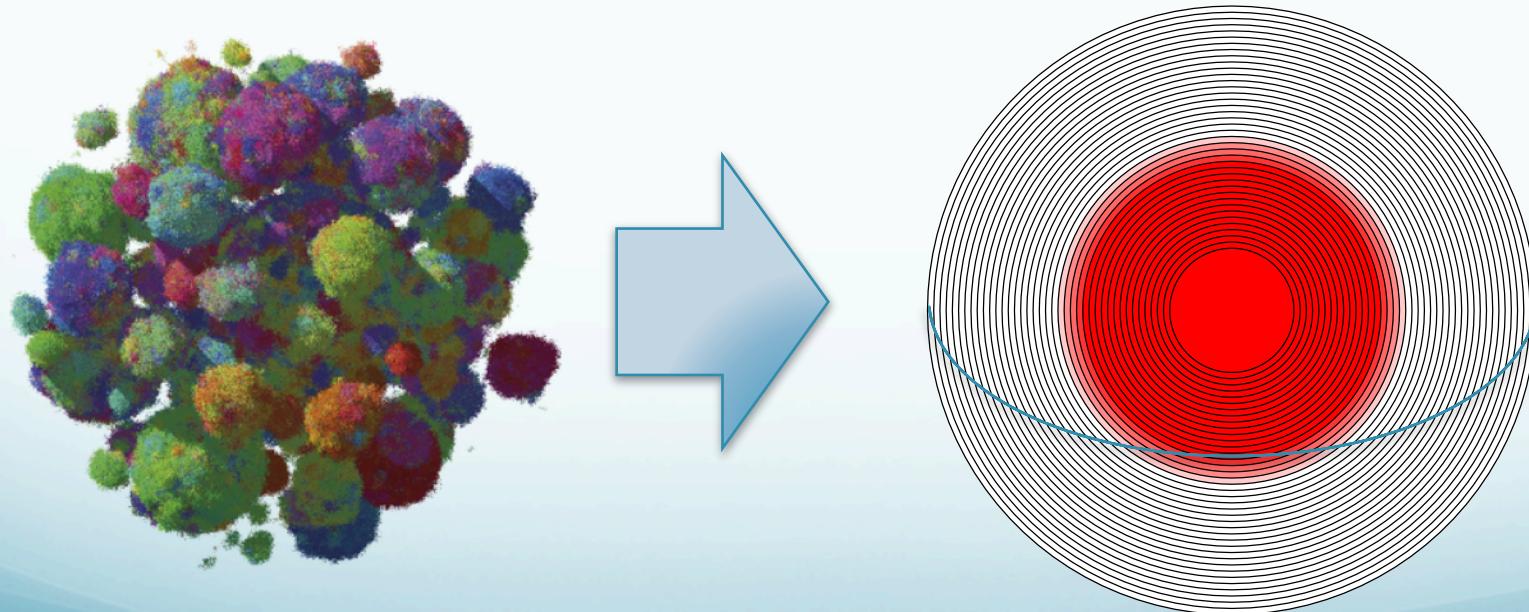
Every Cell represented, grid based.

- Growth (cellular division if space available around + mobility).  
Natural growth of tumor: nbr cells cubic in time.
- Treatment everywhere (e.g. « ray »)
- Treatment in surface (e.g. « medicine »)

# Goal

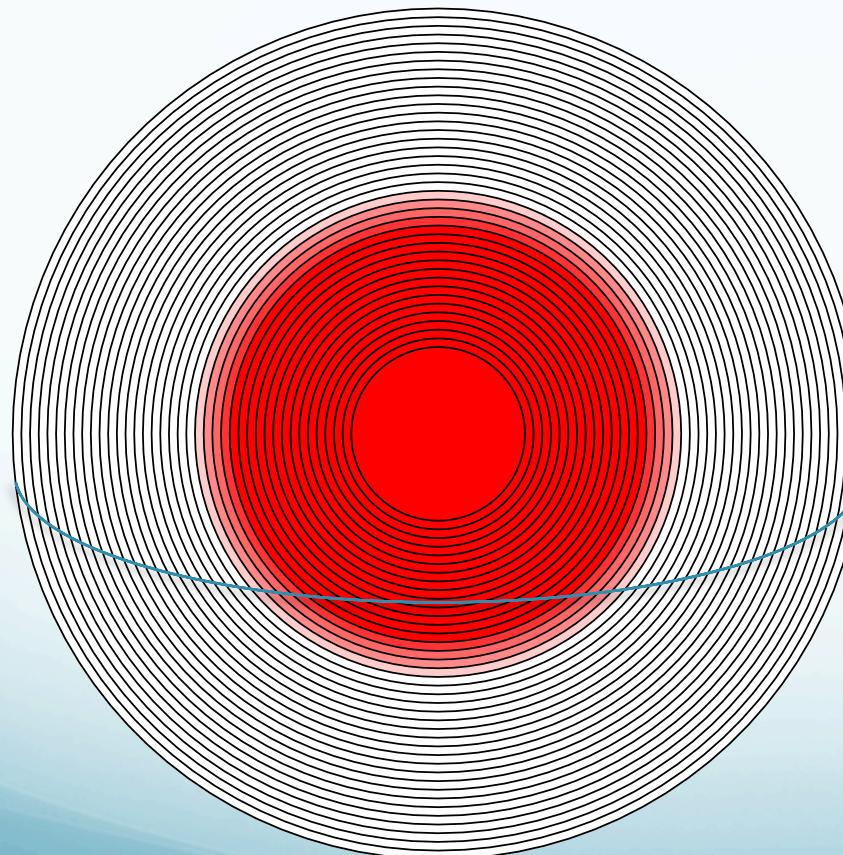
- Obtain a simpler/faster abstraction from Tumor Simulator to evaluate speed of growth/death that does not consider cells individually

If no topological dependencies, easy to obtain equations.  
But growth and surface death depends on positions of cells.



=> Try with «layer»-based model, learnt from statistics

# Our model



40 Layers

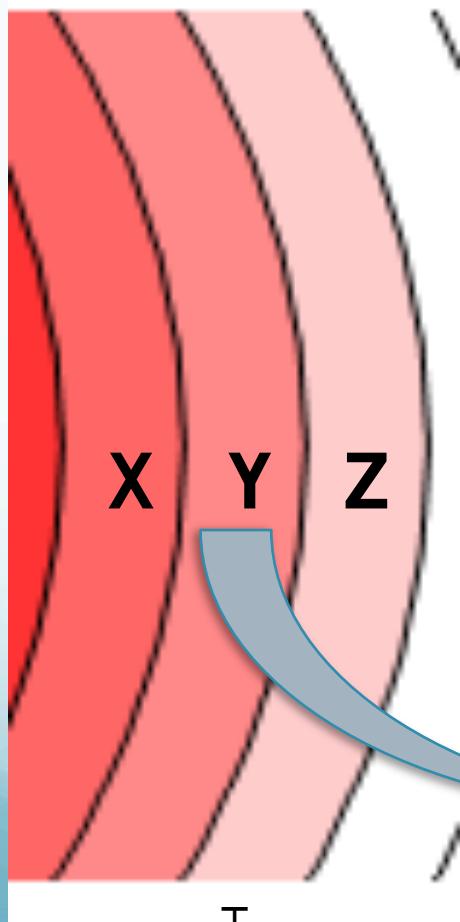
Layers linear with radius  
(Volume of layer is cubic  
as natural growth)

A variable for each layer:  
cell concentration of layer

Can take 100 values

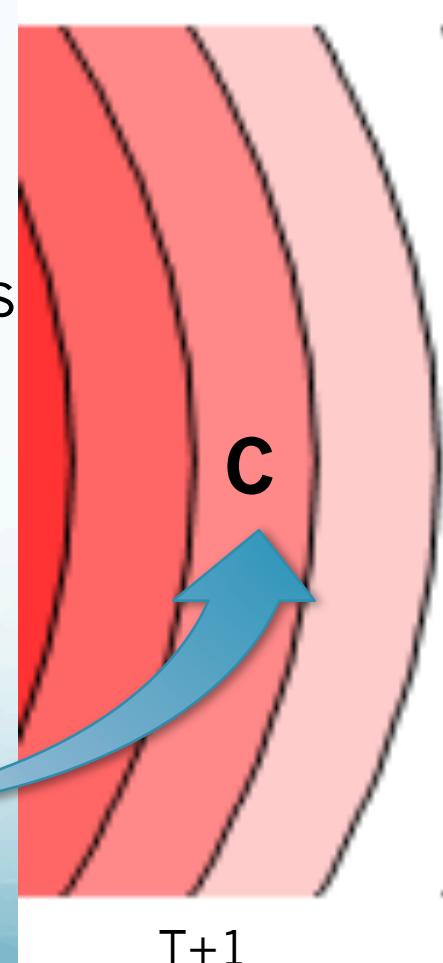
# Probability Tables

Locality : Layer depends on previous, self and next layer



How concentration  
**C** relates to concentrations  
X, Y, Z ?

~5.000 simulations  
to learn  
the « rules »



Rules of the  
form:

For  
X=62  
Y=41  
Z=15

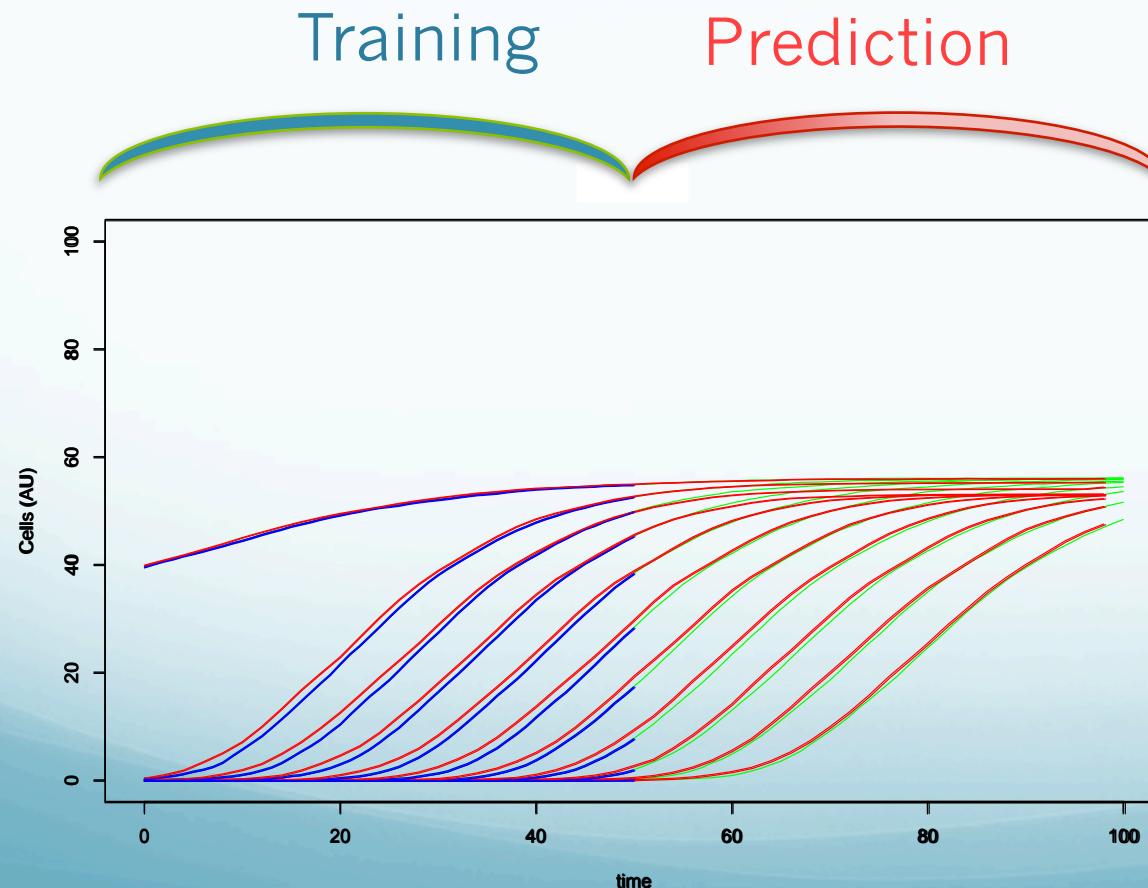
$\text{Prob}(C=52)=0.2$

Rules do not  
depend on  
time or layer.

# Results

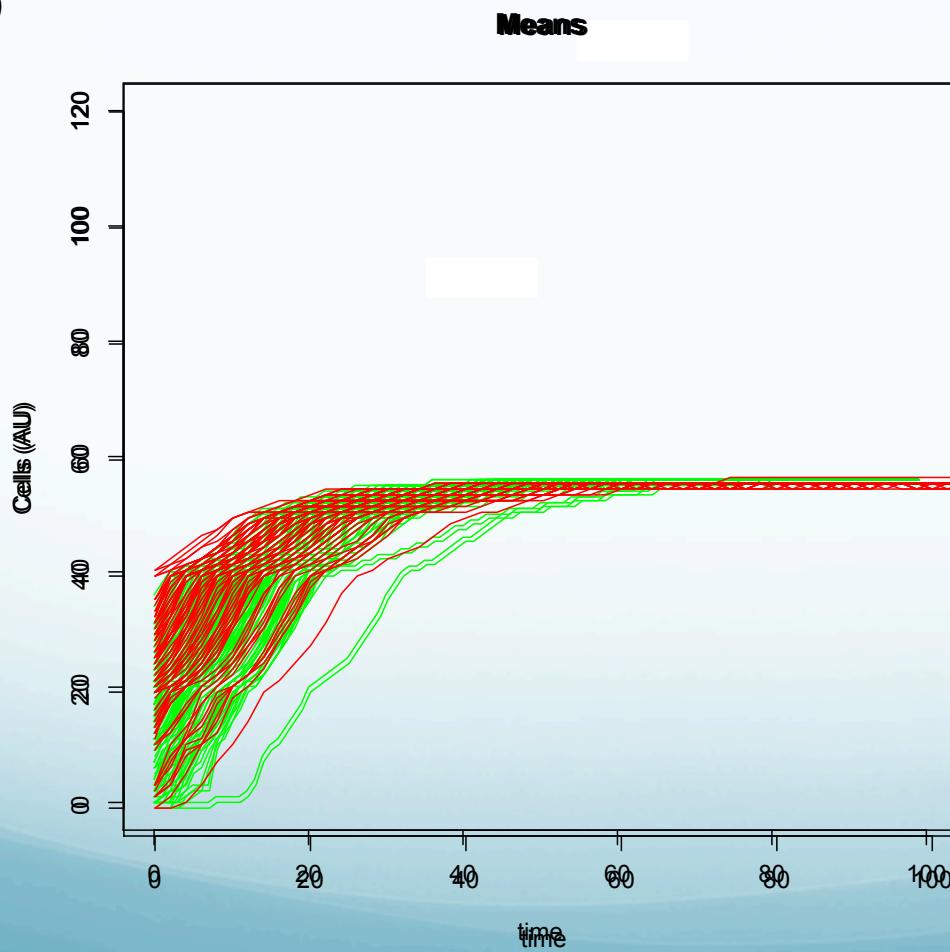
# Results 1: growth (mean)

Growth model (means)



# Growth (distribution)

Growth (100 runs of original and abstraction, Layer 6 )



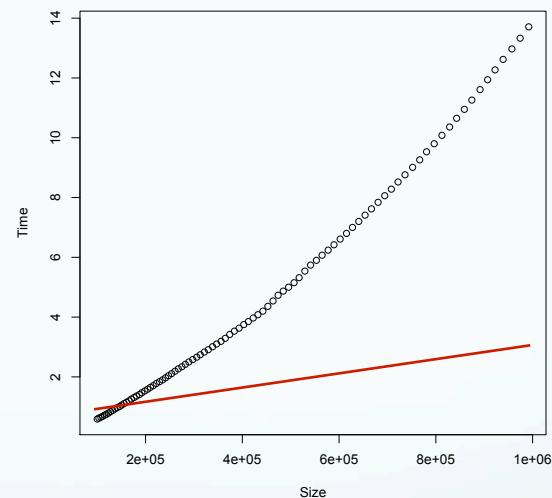
Each run can have a different behavior

Ours seem to match closely the original ones.

# Running Time

Growth till one million cells

- Original : 14.3 seconds
- Our program : 2.46 seconds  
(6X faster)



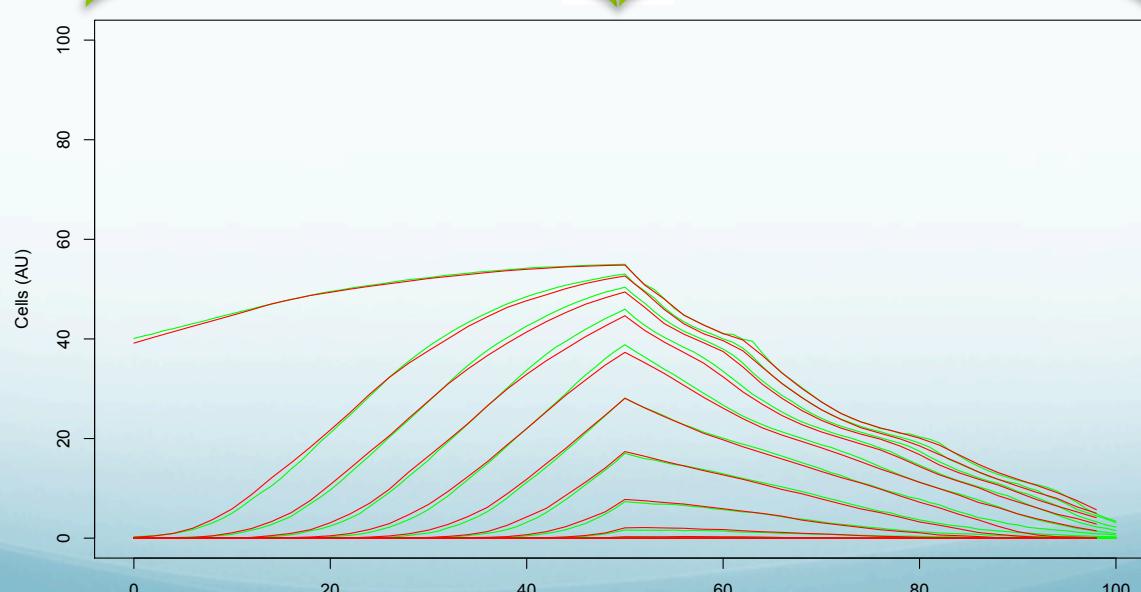
# Results 2: treatment (mean)

Growth model + treatment model

Treatment considered to reach all cells equally (ray)

Growth

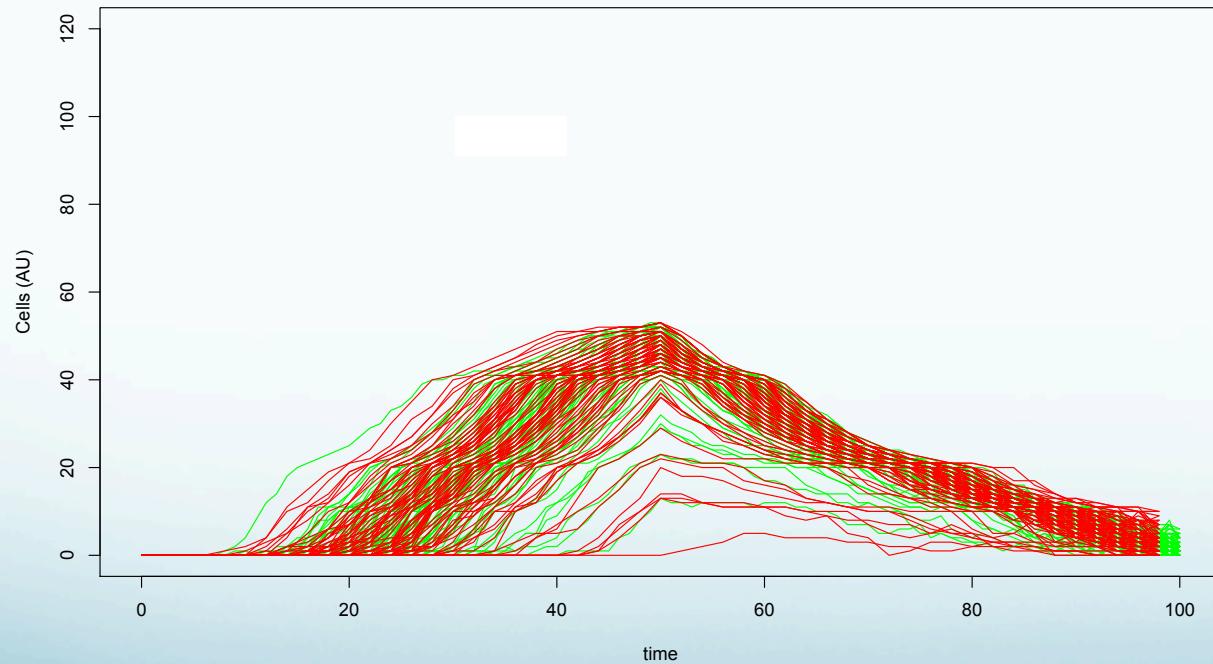
Treatment



Layer abstraction  
is also appropriate  
for treatment

# Treatment (distribution)

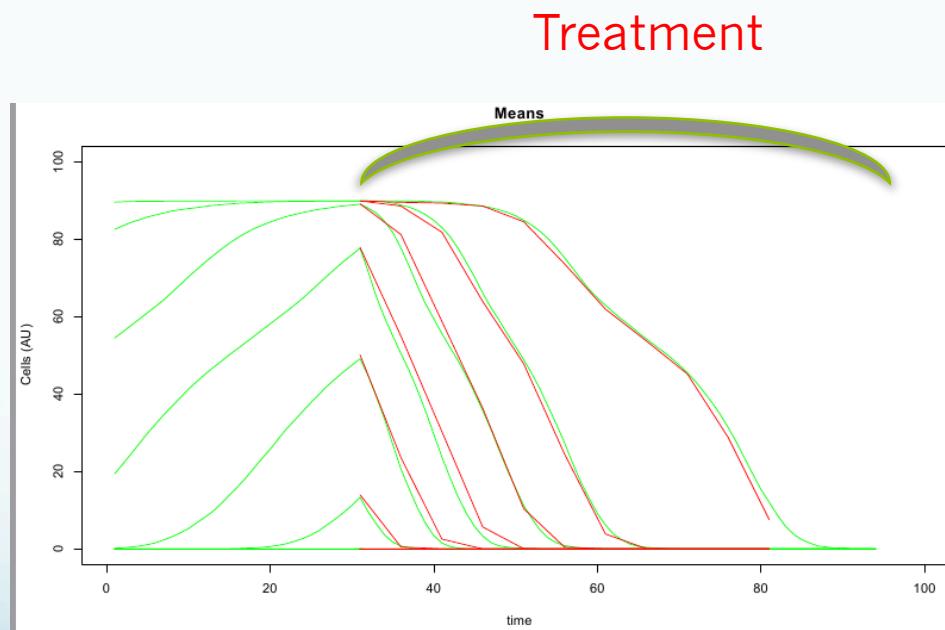
Growth+death ( 100 runs of original and abstraction,  
Layer 3 )



# Results 3: surface treatment

treatment (death on surface)

Treatment reaches the surface cells mostly



Can replay from same configurations

Not enough data yet for better abstraction

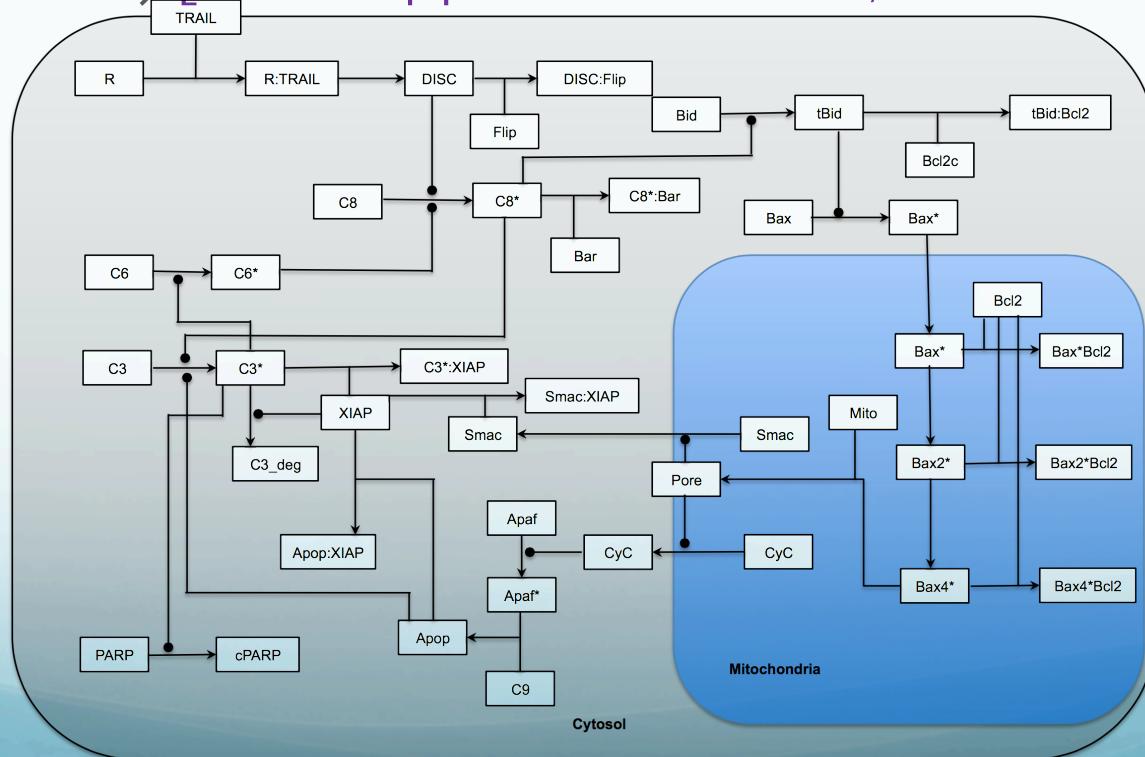
# Future work

# Future work

- Predict outcome of alternations between treatment and no treatment
  - We need more/better data!
  - produced data actively rather than by observation
- Consider more realistic Tumor models
  - (e.g. Drasdo's models)

# Future work

- Consider multi level models (more accurate for treatment):
  - Lower level: treatment with TRAIL (signaling pathway for each cell) [Palaniappan et al. 2017, Bioinformatics]



# Our model

For precision, lots of discretization values

for concentration of layer

=> Two levels of discretization

> High order: 10 values, log scale

0 – 10 – 100 – 1000...

(Optimizing entropy)

> Low order : 10 values, linear scale

